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0110 Intelligenetics  
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FastDB - Fast Pairwise Comparison of Sequences  
Release 5.4

Results file 09-784340-1-q9r110.res made by jdelaval on Sun 2 Sep 101 10:45:02-PDT.

Query sequence being compared:US-09-784-340-1 (1-2759)  
Number of sequences searched: 1  
Number of scores above cutoff: 1

Results of the initial comparison of US-09-784-340-1 (1-2759) with:  
File : q9r110.pep

|       |     |   |   |   |   |   |   |   |   |
|-------|-----|---|---|---|---|---|---|---|---|
| 100-  |     |   |   |   |   |   |   |   |   |
| N     | -   |   |   |   |   |   |   |   |   |
| U     | 50- |   |   |   |   |   |   |   |   |
| M     | -   |   |   |   |   |   |   |   |   |
| B     | -   |   |   |   |   |   |   |   |   |
| E     | -   |   |   |   |   |   |   |   |   |
| R     | -   |   |   |   |   |   |   |   |   |
| O     | 10- |   |   |   |   |   |   |   |   |
| F     | -   |   |   |   |   |   |   |   |   |
| S     | -   |   |   |   |   |   |   |   |   |
| E     | 5-  |   |   |   |   |   |   |   |   |
| Q     | -   |   |   |   |   |   |   |   |   |
| U     | -   |   |   |   |   |   |   |   |   |
| N     | -   |   |   |   |   |   |   |   |   |
| C     | -   |   |   |   |   |   |   |   |   |
| E     | -   |   |   |   |   |   |   |   |   |
| S     | 0-  |   |   |   |   |   |   |   |   |
| SCORE | 0   | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 |
| STDV  |     |   |   |   |   |   |   |   |   |

PARAMETERS

Similarity matrix Unitary K-tuple 2  
Translation Frame 6  
Mismatch penalty 1 Joining penalty 20  
Gap penalty 1.00 Window size 32  
Gap size penalty 0.05  
Cutoff score 1  
Randomization group 0

SEARCH STATISTICS

Scores: Mean 9 Median 0 Standard Deviation 0.00  
Times: CPU 00:00:00.00 Total Elapsed 00:00:00.00  
Number of residues: 530  
Number of sequences searched: 1  
Number of scores above cutoff: 1

The scores below are sorted by initial score.  
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

| Sequence Name | Description                   | Length | Score | Opt. | Stg. | Frame |
|---------------|-------------------------------|--------|-------|------|------|-------|
| 1. q9r110     | UDP GLUCURONOSYLTRANSFERASE U | 530    | 9     | 81   | 0.00 | 1     |

1. US-09-784-340-1 (1-2759)  
q9r110 UDP GLUCURONOSYLTRANSFERASE UGT2A3.

TOIG of: q9r110 check: 732 from: 1 to: 530

ID 09R110 PRELIMINARY; PRT; 530 AA.  
AC 09R110;  
DT 01-MAY-2000 (TEMBREL. 13, Created)  
DT 01-MAY-2000 (TEMBREL. 13, Last sequence update)  
DT 01-MAR-2001 (TEMBREL. 16, Last annotation update)  
DE 01 GLUCURONOSYLTRANSFERASE UGT2A3.  
OS Cavia porcellus (Guinea pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Hystriognathi; Caviidae; Cavia.  
OX NCBI\_TaxID=10141;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=HARTLEY; TISSUE=LIVER;  
RA Smith S.A., Nagalla S.R., Andrews D.P., Olsen G.D.;  
RT "Morphine regulation of a novel uridine diphosphate  
glucuronosyltransferase in guinea pig pups following in utero  
RT exposure.";  
RL Mol. Genet. Metab. 0:0-0(1999).  
DR EMBL; AF175221; AAD51732.1; -  
DR InterPro; IPR002213; -  
DR Pfam; PF00201; UDPGT; 1.  
DR PROSITE; PS00375; UDPGT; 1.  
KW Transferase.  
SQ SEQUENCE 530 AA; 59895 MW; EE2E394D3FD484E1 CRC64;

Q9R110 Length: 530 September 1, 2001 09:56 Type: P Check: 732 ..

Initial Score = 9 Optimized Score = 81 Significance = 0.00  
Residue Identity = 17% Matches = 108 Mismatches = 370  
Gaps = 133 Conservative Substitutions = 0  
Translation Frame = 1

QPIQISVGNCHHEVXQVSPGISAPALLCWLMIMESPGVIALKHEPLAQGSHRSRAHSPRGNSIDSIX  
MAPGLASAVILLILLCAGS-GFCGKYLWPC  
X  
80 90 100 110 120 130 140 150  
AFVNLQFAFCIE--IXGPPATGONRRKXNICXPSSCLARLINLAISYKIKKFFCNRNF-KNDYXELX  
EMSHWLNLKTLLELVKRGHEVT-----VLTLSNLFIDYRHPAF-----NFEVYIPPTDK  
40 50 60 70 80  
150 160 170 180 190 200 210 220 230 240 250 260 270 280 290 300 310 320 330 340 350  
LQSDAYEATGNOLRCNA--YRPGDSLRRPBGYACSPFCAHT--XNFCR-----ROYGAKLWETSSSTFIC  
NMS-----ENILNEFTIELAVNVPMPPLM-QSGKLLQOFFVOITEDLGLNCNRYVYNSLMKRLDSDKYDLV  
90 100 110 120 130 140 150  
T-----CAVDRTRNNDLSGSKSKFNAPSPFLDLSGLRLSFLGRVLAAXGIRKNAHYIMXDGSKXDMANTNI  
TDPVILPGELVAEMIGVPEVNMKLFMSGHTIEKYCGOLPAPSPYVPVPLG--GLTTRMTFMRVKNMYESYL  
160 170 180 190 200 210 220 230 240 250 260 270 280 290 300 310 320 330 340 350  
LGFYSSITPTFLXAYCMRIALXTCSPAXGNGK-----PCPEFGRRYCGVFSGYTVSKYRRKGXHY  
FDFTIOQDYKFMWDOFYSEALGRPTTLCIEIGKAEIWLIRTYWDFEF-PRPYLNFERY-----GGIHL  
230 240 250 260 270 280

|   |     |     |     |     |     |     |
|---|-----|-----|-----|-----|-----|-----|
| 340   | 350 | 360 | 370 | 380 | 390 | 400 |
| CFSCPCDPTEGVMFYQ--RKTIHISQYSAVXLDPRE--XSSMSQSOFPYHSMWMNEMDLXSYLPMGPGYG  |     |     |     |     |     |     |
| CKPAKPLPEKMEEFVQSSGDGVVFLSLSMKYNLTKEEANLIASALQIPOKYLM-----RKQ           |     |     |     |     |     |     |
| 290   | 300 | 310 | 320 | 330 | 340 |     |
| 410   | 420 | 430 | 440 | 450 | 460 |     |
| SSHTWXSXXHHSHHGRRSCRKUL--QNDKRPTEGESHY---RFLXRECETEIKNSP--XSCKA-        |     |     |     |     |     |     |
| ---KKRPTLGPNTRLFDMWIPQNDLGHKPTKAFETHGSSNGCIYEIATHGVMVMCMPLFSQOPDNLGMAK  |     |     |     |     |     |     |
| 350   | 360 | 370 | 380 | 390 | 400 | 410 |
| 470   | 480 | 490 | 500 | 510 | 520 |     |
| -----PRSSL---LDRCHAPQRSQAPALSCXPBHLVPALLYCDWVPADLCNGCYILV-HMFEPT        |     |     |     |     |     |     |
| GAAEVNNNTMTSADLLGALRTYVINDTYENAKLSRIHHDP-----YKPLDRAAFVEVRYMHHKQK       |     |     |     |     |     |     |
| 420   | 430 | 440 | 450 | 460 | 470 |     |
| 530   | 540 | 550 | 560 | 570 | 580 | 590 |
| FLSKLXXMKXKRKRGIDLSFKFKMDLQMXSCXCPBHRIMWKPCEFHITIYVLISXLYSLFEHNEHVASHSF |     |     |     |     |     |     |
| HL-----RVAAHDL-----WFQYHSIDVIGFLACVASAIIILLYRKCLFSFQNTIKIGKRI           |     |     |     |     |     |     |
| 480   | 490 | 500 | 510 | 520 |     |     |
| X   | 610 | 620 | 630 | 640 | 650 | 660 |
| VAFSAVCLLSLJLXHKHDMNTSKSYEXYCHCFHDVITSLSLSDRYCNMLIGVCTNTWMMKSKCKIHKIQ   |     |     |     |     |     |     |
| KKE   |     |     |     |     |     |     |
| 350   |     |     |     |     |     |     |
| 670   | 680 | 690 | 700 | 710 | 720 | 730 |
| XYYQINEAFYDISLXYTXPFENLKKPFYISITDLRQIAKNDRLAHSEFAIEPHPTSSRCHSLHFCH      |     |     |     |     |     |     |
| 750   | 760 | 770 | 780 | 790 | 800 | 810 |
| HLTDIFCVFLMINROFLLSSNKRKNNKFLXKRCRXYDIOKQIILRXVYIRNMKXLPFLIXNFVXXYTYKX  |     |     |     |     |     |     |
| 820   | 830 | 840 | 850 | 860 | 870 | 880 |
| CLFFKMMNTYHNSYLYNQCYNLXKKKNEMLYLKAKKKKKTLSCRYAAYRXPQTYMELRISLTLATLSCRYA |     |     |     |     |     |     |
| YRXQCHALRAYRXQCHAYTXKRYVDSKTTLSAVTX                                     |     |     |     |     |     |     |
| 890   | 900 | 910 |     |     |     |     |

IntelliGenetics

FastDB - Fast Pairwise Comparison of Sequences  
Release 5.4

Results file 09-784340-1-q9r110.res made by jdelaval on Sun 2 Sep 10 10:45:24 -PDT.

Query sequence being compared: US-09-784-340-1 (1-2759)  
Number of sequences searched: 1

Number of scores above cutoff:

Results of the initial comparison of US-09-784-340-1 (1-2759) with:  
File : q9r110.pep

| SCORE | SIDEV |
|-------|-------|
| 0     | 100   |
| 36    | 50    |
| 73    | 50    |
| 109   | 50    |
| 146   | 50    |
| 182   | 50    |
| 219   | 50    |
| 255   | 50    |
| 292   | 50    |
| 328   | 50    |

## PARAMETERS

|                     | Unitary | K-tuple         |
|---------------------|---------|-----------------|
| Similarity matrix   | 6       | 20              |
| Translation frame   | 1       | joining penalty |
| Mismatch penalty    | 0.05    | Window size     |
| Gap penalty         | 0       | 32              |
| Gap size penalty    | 1       |                 |
| Cutoff score        | 0       |                 |
| Randomization group |         |                 |

## SEARCH STATISTICS

|         |             |               |                    |
|---------|-------------|---------------|--------------------|
| Scores: | Mean        | Median        | Standard Deviation |
|         | 328         | 0             | 0.00               |
| Times:  | CPU         | Total Elapsed |                    |
|         | 00:00:00.00 | 00:00:00.00   |                    |

|                                |     |
|--------------------------------|-----|
| Number of residues:            | 530 |
| Number of sequences searched:  | 1   |
| Number of scores above cutoff: | 1   |

The scores below are sorted by initial score. Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

| Sequence Name | Description                   | Length | Score | Opt. Sig. Frame |
|---------------|-------------------------------|--------|-------|-----------------|
| 1. q9r110     | UDP GLUCURONOSYLTRANSFERASE U | 530    | 328   | 387 0.00 2      |

1. US-09-784-340-1 (1-2759)  
q9r110 UDP GLUCURONOSYLTRANSFERASE UGT2A3.

TOIG of: q9r110 check: 732 from: 1 to: 530

ID Q9r110 PRELIMINARY; PRT; 530 AA.  
AC Q9r110:  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
DE UDP GLUCURONOSYLTRANSFERASE UGT2A3.  
OS Cavia porcellus (Guinea pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Hystriocognathi; Caviidae; Cavia.  
OX NCBI\_Taxid=10141;  
RN (1)  
RP SEQUENCE FROM N.A.  
RC STRAIN=HARTLEY; TISSUE=LIVER;  
RA Smith S.A., Nagalla S.R., Andrews D.P., Olsen G.D.;  
RT "Morphine regulation of a novel uridine diphosphate  
RT glucuronosyltransferase in guinea pig pups following in utero  
RT exposure";  
RL Mol. Genet. Metab. 0:0-0(1999).  
DR EMBL; AF175221; AAD51732.1; -.  
DR InterPro: IPR002213; -.  
DR Pfam: PF00201; UDPGT; 1.  
DR PROSITE; PS00375; UDPGT; 1.  
KW SEQUENCE.  
SQ SEQUENCE 530 AA; 59895 MM; EE2F394D3FDA84E1 CRC64;

Q9r110 length: 530 September 1, 2001 09:56 Type: P Check: 732

Initial Score = 328 Optimized Score = 387 Significance = 0.00  
Residue Identity = 71% Matches = 378 Mismatches = 149  
Gaps = 3 Conservative Substitutions = 0  
Translation Frame = 2

|  |     |     |     |     |     |     |    |
|--|-----|-----|-----|-----|-----|-----|----|
| 10   | X   | 20  | 30  | 40  | 50  | 60  | 70 |
| NHCRSVCEGTALMRSDKSLVFLQLFCVGGCGKVLWPCDMSHMLNVRVILEELIVRGHEVTVLTHSK           |     |     |     |     |     |     |    |
| 1  | 1   | 1   | 1   | 1   | 1   | 1   | 1  |
| MAGKILASAVALLLLCCAGSGFCGKVLWPCDMSHMLNKTLLLEELIVRGHEVTVLTHSK                  |     |     |     |     |     |     |    |
| X  | 10  | 20  | 30  | 40  | 50  | 60  | 60 |
| 80   | 90  | 100 | 110 | 120 | 130 | 140 |    |
| PSLIDYRKPSALKEFEVYHHPD-RTEEN--EIFVDIALNVLPGSLTWSVIRKLNDFEVEIRGTLMKMCESFI     |     |     |     |     |     |     |    |
| 1  | 1   | 1   | 1   | 1   | 1   | 1   | 1  |
| NLFIDYNRHAPAFNEFVIAPPTDKNMSSENLNFIELAVVMPMTPLMOSGKLLQOFVOITEDLGINCRNTV       |     |     |     |     |     |     |    |
| 70   | 80  | 90  | 100 | 110 | 120 | 130 |    |
| 150  | 160 | 170 | 180 | 190 | 200 | 210 |    |
| YNQTLMKKLTQETNYDVMILDPVIPCGLDIAELLAAVPEVTLIRISVGNMNRSCGKLPAPLASVVPVPMGLTD    |     |     |     |     |     |     |    |
| 1  | 1   | 1   | 1   | 1   | 1   | 1   | 1  |
| YNOSLMKRLRDSKYDVLVTDVYIPCGELVAEMLVGPEVNMVKFSMGHTIEKVCGLDLPAPPSVVPVPLGLTT     |     |     |     |     |     |     |    |
| 140  | 150 | 160 | 170 | 180 | 190 | 200 |    |
| 220  | 230 | 240 | 250 | 260 | 270 | 280 |    |
| RMTFLERKNSMLSVLFFHFWIQDYDHFHWEFFYSKALGPTTLCEITVGKAEIWLIRTYWDFEFPQYOPNFE      |     |     |     |     |     |     |    |
| 1  | 1   | 1   | 1   | 1   | 1   | 1   | 1  |
| RMTFMERKYNMVFSLVLFDFWIOQDYKFWMDQYSEALGPTTLCEITVGKAEIWLIRTYWDFEFPQYOPNFE      |     |     |     |     |     |     |    |
| 210  | 220 | 230 | 240 | 250 | 260 | 270 |    |
| 290  | 300 | 310 | 320 | 330 | 340 | 350 |    |
| FVGGILHCRPAKALPKREMEFVOSSEGDGIVFSLGSLFQNTVEERANIIASALAQIPQKVLIMRYKGRKRPSTL   |     |     |     |     |     |     |    |
| 1  | 1   | 1   | 1   | 1   | 1   | 1   | 1  |
| FVGGILHCRPAKPLPKREMEFVOSSEGDGIVFSLGSLMVKNIITEERANIIASALAQIPQKVLIMRYKGRKRPATL |     |     |     |     |     |     |    |

|   |     |     |     |     |     |     |     |
|---|-----|-----|-----|-----|-----|-----|-----|
| 280   | 290 | 300 | 310 | 320 | 330 | 340 |     |
| 360   | 370 | 380 | 390 | 400 | 410 | 420 |     |
| GANTLTYDMIPQNDLLGHPKKAFTTHGGMNGIYAIYHGVPMVGPPIFGQDLNDIAHMAKGAVEINFKT    |     |     |     |     |     |     |     |
| 1   | 1   | 1   | 1   | 1   | 1   | 1   | 1   |
| GNTELFWMIPQNDLLGHPKKAFTTHGGMNGIYAIYHGVPMVGPPIFGQDLNDIAHMAKGAVEINFKT     |     |     |     |     |     |     |     |
| 350   | 360 | 370 | 380 | 390 | 400 | 410 | 420 |
| 430   | 440 | 450 | 460 | 470 | 480 | 490 | 500 |
| MISEDLALRRTVITDSSYKENAMRLSRHHDPYKPLDRAVFWIEFVNRHKGAKHLASAADLTWPGHYST    |     |     |     |     |     |     |     |
| 1   | 1   | 1   | 1   | 1   | 1   | 1   | 1   |
| MTSADLGLALRTVINDPYKENAMRLSRHHDPYKPLDRAVFWIEFVNRHKGAKHLASAADLTWPGHYST    |     |     |     |     |     |     |     |
| 430   | 440 | 450 | 460 | 470 | 480 | 490 |     |
| DVIGFLTCVATAIPLFTKCPFCSCQKNKTRIKERKREIFPNSRKTWGNPNVNSHIEPGENLAIFLTLSTL  |     |     |     |     |     |     |     |
| 1   | 1   | 1   | 1   | 1   | 1   | 1   | 1   |
| DVIGFLTCVATAIPLFTKCPFCSCQKNKTRIKERKREIFPNSRKTWGNPNVNSHIEPGENLAIFLTLSTL  |     |     |     |     |     |     |     |
| 500   | 510 | 520 | 530 | 540 | 550 | 560 | 570 |
| LFYLSYIAKNSMIMRLXYLLSLHFPKCAVSLSLCOTRTYIHILNFPISDITVYMTSLLXPRYIGRPAIC   |     |     |     |     |     |     |     |
| 580   | 590 | 600 | 610 | 620 | 630 | 640 |     |
| 650   | 660 | 670 | 680 | 690 | 700 | 710 |     |
| XFLVFAQTHGCKEVENNVKFTKSPKSKMSMTLACYEXHNDFFSIXISPSTYPALLISDNDLKMTHIG     |     |     |     |     |     |     |     |
| 720   | 730 | 740 | 750 | 760 | 770 | 780 |     |
| YQNSULAFHPIHPLVIAVIAISITVLTFFVCSXXXIDSSYCPQIIEKTEFLHLENVHKIFKLNRLFXDKX  |     |     |     |     |     |     |     |
| 790   | 800 | 810 | 820 | 830 | 840 | 850 | 860 |
| PLEICDCNEXFYKILIDSTLDLNVYSLKXXLILILISIIKSIYCRKIKRCLFXXXXKKKKKHCHAVYXRIY |     |     |     |     |     |     |     |
| 870   | 880 | 890 | 900 | 910 |     |     |     |
| DSPLSCRYIAVYKXQNHCAVYKRIYDSTVMERIEIVDSTVMPLRKSVSLFAKHCOPLRS             |     |     |     |     |     |     |     |

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FastDB - Fast Pairwise Comparison of Sequences  
Release 5.4

Results file 09-784340-1-q9r110.res made by jdelaval on Sun 2 Sep 101 10:45:46-PDT.

Query sequence being compared: US-09-784-340-1 (1-2759)  
Number of sequences searched: 1  
Number of scores above cutoff: 1

Results of the initial comparison of US-09-784-340-1 (1-2759) with:  
File : q9r110.pep

100-  
N -  
U 50-  
M -  
B -  
E -  
R -  
O -  
F 10-  
S -  
E 5-  
Q -  
U -  
E -  
C -  
N -  
E -  
S 0-  
SCORE 0 1 2 3 4 5 6 7  
STDEV

PARAMETERS

Similarity matrix Unitary 2  
Translation Frame 6  
Mismatch penalty 1 Joining penalty 20  
Gap penalty 1.00 Window size 32  
Gap size penalty 0.05  
Cutoff score 1  
Randomization group 0

SEARCH STATISTICS

Scores: Mean 7 Median 0 Standard Deviation 0.00  
Times: CPU 00:00:00.00 Total Elapsed 00:00:00.00

Number of residues: 530  
Number of sequences searched: 1  
Number of scores above cutoff: 1

The scores below are sorted by initial score.  
Significance is calculated based on initial score.  
A 100% identical sequence to the query sequence was not found.

The list of best scores is:

| Sequence Name | Description                   | Length | Score | Opt. | Sign. | Frame |
|---------------|-------------------------------|--------|-------|------|-------|-------|
| 1. q9r110     | UDP GLUCURONOSYLTRANSFERASE U | 530    | 7     | 85   | 0.00  | 3     |

1. US-09-784-340-1 (1-2759)  
q9r110 UDP GLUCURONOSYLTRANSFERASE UGT2A3.

TOIG of: q9r110 check: 732 from: 1 to: 530

ID 09r110 PRELIMINARY; PRT; 530 AA.  
AC 09r110;  
DT 01-MAY-2000 (TREMblrel. 13, Created)  
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)  
DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)  
DE UDP GLUCURONOSYLTRANSFERASE UGT2A3.  
OS Cavia porcellus (Guinea pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Hystriognathi; Caviidae; Cavia.  
OX NCBI\_TaxID=10141;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=HARTLEY; TISSUE=LIVER;  
RA Smith S.A., Nagalia S.R., Andrews D.P., Olsen G.D.;  
RT "Morphine regulation of a novel uridine diphosphate  
glucuronosyltransferase in guinea pig pups following in utero  
RT exposure.";  
RL Mol. Genet. Metab. 0:0-0(1999).  
DR EMBL; AF175221; AAD51732.1;  
DR InterPro; IPR002213;  
DR Pfam; PF00201; UDPGT; 1.  
DR PROSITE; PS00375; UDPGT; 1.  
KW Transferase.  
SQ SEQUENCE 530 AA; 59895 MW; EE2F394D3FD484E1 CRC64;

Q9r110 Length: 530 September 1, 2001 09:56 Type: P Check: 732

Initial Score = 7 Optimized Score = 85 Significance = 0.00  
Residue Identity = 18% Matches = 112 Mismatches = 363  
Gaps = 134 Conservative Substitutions = 0  
Translation Frame = 3

TIADQCVRELPSXGLTSQLWYFCSSSVLAVDYGVKSWCGPVTXAIGMRSFYKSSXXEMRXOXYLTOS  
10 20 30 40 50 60 70  
80 90 100 110 120 130 140  
LRLTLTGLLHXLNLRMSICHRTEOKRMKYLTLXLMSCAAYOPGNOLNKMIFLLKXELKXXCVRALSTIR  
150 160 170 180 190 200 210  
RLKRSYRKPTTMKCLXTLFPVETXWLSCLQSILCSHLEFLKALWSEAVNGFOLHPNYLCLXODXOTEXP  
MARGKL-----  
X  
220 230 240 250 260 270 280  
FMKEKKIQCFQFCSTSGFRITITIFGKSEIVRHXE--GPLHYVRIMKIRGYXHEIGILNLTNTLS-  
--ASAVALLLLLCCAGSGF-----CGK-VLWVPCESHWLNKLTLEELVKGHE-----VTVALTSLN  
10 20 30 40 50 60  
290 300 310 320 330 340  
-LLED-----CTVNLPRKLCRLKWKILSRVQGMVLMCFWGHCFKMLQKRLIS--LLO-----PLPRSH  
NLFIDYNRPAPFNEFVIYPPVTDKNMS-----ENILNFIELAVNAVMTPLMOSGKLQDFVOITEDGLNC  
70 80 90 100 110 120  
350 360 370 380 390 400  
R-RCYGGTKEKNHPXEPILGCMIGYPRMIFLYIPKPKLLSLM-VEKXGSMALFTMG-----SLMWEPFY  
RNTVYNGSLMK-----KLKDSKYDVLVTDPIVPCGELVAEMLGVFVNMMLKFSKGMTIERCYGQQLPAPS

|   |   |                           |     |     |     |     |
|---|---|---------------------------|-----|-----|-----|-----|
| 130   | 140   | 150                       | 160 | 170 | 180 | 190 |
| 410   | 420   | 430                       | 440 | 450 | 460 | 470 |
| LVIISLTLXLTJR--   | PKEOJLXKXSKLXOAKIYXJLXEOSELPILIKRMLNDYOFTMINIXSPXIEOSSGSS |                           |     |     |     |     |
| YVPVPLGLGTLTBMTEMERKXNMFVSLXDFEWI-----  | QOYDKFMDQFYSALGRPTLCEIMGKAETI                             |                           |     |     |     |     |
| 200   | 210   | 220                       | 230 | 240 | 250 |     |
| 480   | 490   | 500                       | 510 | 520 | 530 |     |
| SJSCAKKEPSTCDQJLPMTPSSSTJLXMKJGSCXPMOL-----                                   | LYSCSONVFYF---PYKNILIKTER                                 |                           |     |     |     |     |
| WL-----   | IRTWDEEFPAPRYLPNFEFVGJLHCKRPKPEKEEFOYSSGDDGVVYSJGSMVKNL-- | TEEE                      |     |     |     |     |
| 260   | 270   | 280                       | 290 | 300 | 310 | 320 |
| 540   | 550   | 560                       | 570 | 580 | 590 | 600 |
| KXRGNSFOIOERPGVILILPATXNLVKLTLESTYLLFCYFIILAIKXIPRIYKXGCEYISFRCJFLGVLLTF      |   |                           |     |     |     |     |
| KANLIASALAQ--IPQKV--  | LMRRYKXKKRPATLGPNRLLF-----                                | DWIPQNDLGHCKTKAFITGSSNGCI |     |     |     |     |
| 330   | 340   | 350                       | 360 | 370 | 380 |     |
| 610   | 620   | 630                       | 640 | 650 | 660 |     |
| SHPFVQGHYEYLIIFFLISLFP-----   | XHHYFNSLKKXXDDLOYADSWCLHHKHMDVKKKMXKXNSONS                |                           |     |     |     |     |
| YEAIIYHGVPMVQMPIF--   | SDQPDNLGAKMKAKGAAEVNMNMTWSADLLGAA--                       | LRVYINDPTYENAMKLS         |     |     |     |     |
| 390   | 400   | 410                       | 420 | 430 | 440 |     |
| 670   | 680   | 690                       | 700 | 710 | 720 | 730 |
| VHMTNOXSLIHXLYMSNMJLTFQFKKA--   | LLHTOHYXSOTMCKKKXKXGITLIVCYISTYLIXMSXPTFF                 |                           |     |     |     |     |
| RJHHND--  | PVKPDLRAAEVFEVPMNHKGAKNHJRVANHDLSPFOYHSLDVIGFL--          | ACVASAILLVTKCGLFE         |     |     |     |     |
| 450   | 460   | 470                       | 480 | 490 | 500 | 510 |
| 740   | 750   | 760                       | 770 | 780 | 790 | 800 |
| LPSLXNHFLCYVLDKXKYLLIYLKXKKKKKIKFSEIEMKSIRSSXNDYFEISNHKKUYVIVISDFIKFKXLIYHL   |   |                           |     |     |     |     |
| -SFONFIKIGKRRIKE  |   |                           |     |     |     |     |
| 520   | 530   |                           |     |     |     |     |
| 810   | 820   | 830                       | 840 | 850 | 860 | 870 |
| IXMSILXNDZEYXPLSLKSKXVAFYVEKKRBDACSESKKKKKKNVTWPLRKSYSVLTALCHAVTJHIVDSIDVYMLP |   |                           |     |     |     |     |
| 880   | 890   | 900                       | 910 |     |     |     |
| RSVSLTALSCTVSVSLTALSCRYVAYRKQONTVSRYYA  |   |                           |     |     |     |     |

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 01 | 0  
 > 0 <

FastDB - Fast Pairwise Comparison of Sequences  
 Release 5.4

Results file 09-784340-1-q9r110.res made by jdelaval on Sun 2 Sep 10 10:46:00-PDT.

```

query sequence being compared:US-09-784-340-1 (1-2759)
Number of sequences searched: 1
Number of scores above cutoff: 1

```

Results of the initial comparison of US-09-784-340-1 (1-2759) with:  
File : q9r110.pep

|       |     |
|-------|-----|
| N     | -   |
| U     | 50- |
| M     | -   |
| B     | -   |
| E     | -   |
| R     | -   |
| O     | 10- |
| F     | -   |
| S     | -   |
| E     | 5-  |
| O     | -   |
| D     | -   |
| E     | -   |
| N     | -   |
| C     | -   |
| E     | -   |
| S     | 0-  |
| SCORE | 0   |
| STDEV | 1   |
|       | 1   |
|       | 2   |
|       | 2   |
|       | 3   |
|       | 4   |
|       | 5   |
|       | 5   |
|       | 6   |
|       | 7 * |

## PARAMETERS

|                     | Unary | K-tuple |
|---------------------|-------|---------|
| Similarity matrix   | 6     | 20      |
| Translation frame   | 1     | 32      |
| Mismatch penalty    | 1.00  |         |
| Gap penalty         | 0.05  |         |
| Gap size penalty    |       |         |
| Cutoff score        | 0     |         |
| Randomization group | 0     |         |

SEARCH STATISTICS

| Scores: | Mean | Median | Standard Deviation |
|---------|------|--------|--------------------|
|         | 7    | 0      | 0.00               |

| Times:      | CPU         | Total Elapsed |
|-------------|-------------|---------------|
| 00:00:00.00 | 00:00:00.00 | 00:00:00.00   |

00:00:00:00

Number of residues: 530

Number of scores above cutoff: 1

The scores below are sorted by initial score. Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found

The list of best scores is:

| Sequence Name | Description                   | Length | Score | Opt. Frame | Sig.   |
|---------------|-------------------------------|--------|-------|------------|--------|
| 1. q9r110     | UDP GLUCURONOSYLTRANSFERASE U | 530    | 7     | 82         | 0.00 4 |

1. US-09-784-340-1 (1-2759)  
q9r110 UDP GLUCURONOSYLTRANSFERASE UGT2A3.

TOIG of: q9r110 check: 732 from: 1 to: 530

ID 09r110 PRELIMINARY: PRT: 530 AA.  
AC 09r110:  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DE 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
DE UDP GLUCURONOSYLTRANSFERASE UGT2A3.  
OS Cavia porcellus (Guinea pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Hystriognath; Cavidae; Cavia.  
OX NCBI\_Taxid=10141;  
RN (1)  
RP SEQUENCE FROM N.A.  
RC STRAIN=HARTLEY; TISSUE=LIVER;  
RA Smith S.A., Nagalla S.R., Andrews D.P., Olsen G.D.;  
RT Morphine regulation of a novel uridine diphosphate  
RT glucuronosyltransferase in guinea pig pups following in utero  
RT exposure.;  
RL Mol. Genet. Metab. 0:0-0(1999).  
DR EMBL: AF175221; AAD51732.1; -;  
DR InterPro: IPR002213; -;  
DR Pfam: PF00201; UDPGT; 1.  
DR PROSITE: PS00375; UDPGT; 1.  
KW Transferase.  
SQ SEQUENCE 530 AA: 59895 MW: EE2F394D3FD484E1 CRC64;

Q9r110 Length: 530 September 1, 2001 09:56 Type: P Check: 732 ..

Initial Score = 7 Optimized score = 82 Significance = 0.00  
Residue Identity = 184 Matches = 109 Mismatches = 354  
Gaps = 134 Conservative Substitutions = 0  
translation Frame= 4

RYVADVSLSTIRVFAKCCORRYARNAKCCORATXRHDSYAVNDMLRNGMTVGCQRATXRHDSVFFF  
80 90 100 110 120 130 140  
FFFTFRISLSFFYSKLYFLKRLKELVFIILKNRHLNQVYQLEFYKIRNYNHIFLWVYLIKILCLTXISY  
150 160 170 180 190 200 210  
GHFLYVRKFOFLLEFDNNKNCFLTIKNTOKMSYKWKCKRLHLDVCGNIANYSECNALSSFLAIHCLRS  
MARGKLAS  
X

220 230 240 250 260 270 280  
VNLGKMKGLFKLKKNHYTHNKL-----MSXNASLICVYVYIILKILHFLLLYTH-VFVOT--PGISILQVT  
AVL-----LLILCCAGSGCGKVLVWPCSMHMLN-----KTLLELVKRGHEVTVLLISNMLFTDYNR  
10 20 30 40 50 60  
290 300 310 320 330 340  
LSLKVREVTSMKQYOKXENLDVPSLCHKY--REESHKTXENMTKREKDLFTSXSWSNR-----LYSXD-  
HPAFNEFVIVPPTDKMSENILNEFTEIAVNVWPTVLMQSGKLLQGFVQVOTEDGLNCRNTVYNQSLMKK  
70 80 90 100 110 120 130 140

350 360 370 380 390 400  
ITEXILKKKXGFOHILCGNMKODYIRSLFLN-LERS-----IPSLSEFYXIFDRKIRNIIATRI  
LRDSKYDVLTDPVIPCGLVAMGLVFPVNMKLSMGHTIEKYGQLPAPPS-----YVPVPLGLLTRM

150 160 170 180 190 200  
410 420 430 440 450 460 470  
XQLPHRSAGTOSHLSXSGTRXGCHGOLLGAMLLCGAXOTRSRRLDLGALQYDNG--EFLISXHSILYKRN  
TIPHERKNNWFSYL-----FDFWIOQYDKFW-----DOFYSALGRPTTLEINGKRAEITWIRTYWDEFP  
210 220 230 240 250 260  
480 490 500 510 520 530  
RXXLFSKPSV-NLRLSXFXSL-----FLQ-----LLIMPSCCLCYQADHQIWLPPXGPHGXLR  
RPYLPNFEFVYGLHCKPAKPLPKEMEEFVQSGEDGVVVFSGSMVKNLTEKANIILASALQIP-QKVLNR  
270 280 290 300 310 320 330  
540 550 560 570 580 590  
-----SHSFHEHXXKLMFWDDQEDHSVSNHTAIEYLLMMWVFLCTSIPTPSVSGGGLKQXYXPFLLXHFET  
YKGRKPATLGPNTFLFDWIPQNDLIGHPKTKA-----FIT-HGSGNGIEAIV-----  
340 350 360 370 380 390  
600 610 620 630 640 650 660  
VTPPEKTPQYHPLPMSGO--NPFPPXAKIMQY-----YSAILOQOTSXVGVNBEIQNPMEVLAISOLEPQ  
--HGVPVWGPFIISDQDNLGAKKAGCAVEVNMNTTSADLIGALRTVINDPYKENAMKLSRIHHQDPV  
390 400 410 420 430 440 450  
670 680 690 700 710 720  
SHIMXWAF-----LMYYKTL--PKNDSRNPESRSGTKLKNLNFLEPERSFCLLVLSXQVHRKVEVLS  
KPLDRAATWVEFVNHKAKKHLRYAANHLMSWFOYS--LDVIGFLACVASAILLV-----TKCLPSF  
460 470 480 490 500 510  
730 740 750 760 770 780 790  
HSFAFYCLQKFXVXAKQGLQATOPSGLHRESQGLXALHRSWFPVASSXASDCXSSHTSLKRLPQOKNH  
ONFIRIKGRRIKKE  
520 530  
800 810 820 830 840 850 860  
LILXILARLISLARHSELGQIFHFLPCPVAYGPPQJISMOKASQSLTKALSESILLPHQLSLXALLEXPX  
870 880 890 900 910  
HANGSCHRAITGLSHRHISQHRRAAGAEIPKLTQTSXWCPPTLIGN

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> 0 <

FastDB - Fast Pairwise Comparison of Sequences  
Release 5.4

Results file 09-784340-1-q9r110.res made by jdelaval on Sun 2 Sep 101 10:46:10-PDT.

Query sequence being compared: US-09-784-340-1 (1-2759)  
Number of sequences searched: 1  
Number of scores above cutoff: 1

Results of the initial comparison of US-09-784-340-1 (1-2759) with:  
File: q9r110.pep

100-  
N -  
U 50-  
M -  
B -  
E -  
R -  
O 10-  
F -  
S -  
O 5-  
O -  
U -  
E -  
N -  
C -  
E -  
S 0-  
SCORE 0 1 1 2 2 3 3 4 4 5  
SIDEV

## PARAMETERS

Similarity matrix Unitary k-tuple 2  
Translation Frame 6  
Mismatch penalty 1 Joining penalty 20  
Gap penalty 1.00 Window size 32  
Gap size penalty 0.05  
Cutoff score 1  
Randomization group 0

## SEARCH STATISTICS

Scores: Mean 5 Median 0 Standard Deviation 0.00  
Times: CPU 00:00:00.00 Total Elapsed 00:00:00.00  
Number of residues: 530  
Number of sequences searched: 1  
Number of scores above cutoff: 1

The scores below are sorted by initial score.  
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

| Sequence Name | Description                   | Length | Score | Opt. | Sig. | Frame |
|---------------|-------------------------------|--------|-------|------|------|-------|
| 1. q9r110     | UDP GLUCURONOSYLTRANSFERASE U | 530    | 5     | 72   | 0.00 | 5     |

1. US-09-784-340-1 (1-2759)  
q9r110 UDP GLUCURONOSYLTRANSFERASE UGT2A3.

TOIG of: q9r110 check: 732 from: 1 to: 530

ID 09r110 PRELIMINARY; PRT; 530 AA.  
AC 09r110.  
DT 01-MAY-2000 (TREMblrel. 13, Created)  
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)  
DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)  
DE UDP GLUCURONOSYLTRANSFERASE UGT2A3.  
OS Cavia porcellus (Guinea pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Hystriognathi; Caviidae; Cavia.  
OX NCBI\_TaxID=10141;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=HARTLEY; TISSUE=LIVER;  
RA Smith S.A., Nagalia S.R., Andrews D.P., Olsen G.D.;  
RT "Morphine regulation of a novel uridine diphosphate  
glucuronosyltransferase in guinea pig pups following in utero  
exposure.";  
RL Mol. Genet. Metab. 0:0-0(1999).  
DR EMBL; AF175221; AAD51732.1; -  
DR InterPro: IPR002213; -  
DR Pfam; PF00201; UDPGT; 1.  
DR PROSITE; PS00375; UDPGT; 1.  
KW Transferase.  
SQ SEQUENCE 530 AA; 59895 MW; EE2F394D3FDD484E1 CRC64;

09r110 Length: 530 September 1, 2001 09:56 Type: P Check: 732 ..

Initial Score = 5 Optimized Score = 72 Significance = 0.00  
Residue Identity = 18% Matches = 92 Mismatches = 318  
Gaps = 101 Conservative Substitutions = 0  
Translation Frame= 5

ATXRLTVCCQRYATXRHDSAVNDTLVTHDSAVNDTLRNGMTVSLTICVYTAQXMAVNDTLRNGMTVFFFE  
80 90 100 110 120 130 140  
FFLASEQSLVSTVNYTFEDYDKNKEYSSFRIDIXIKCTINXNFISEITFYFWMLLSKSXVLEVLM  
150 160 170 180 190 200 210  
DIFSXXENSFYYLRTIIRFVYLSSTRHKKCOLSDGRNNGVDIMRYVEIXOTLLSWPVRHFXQPIVXQ  
220 230 240 250 260 270 280  
XCMVCRAVYLNKKRIIMLLTSXCHRMILXKFWTFEPCFEYIFFTSMCLCKHQSAYCSPYHLRLKRX  
290 300 310 320 330 340 350  
XKHGNSDIRNRKRIKMYSCPCVTKKXKRVSTPRKMKRKNELYSQPHDGIILGIIAKIKQNRKXENSKYFTKF  
360  
YVAGINRITPSGLSXIMWDLPLFLYLSFIFLTKGKXKTFCEQESCHTGOQEPNHITRYRVLEPGEVWGSX  
370 380 390 400 410 420 430  
440 450 460 470 480 490 500  
SOVLGSPVAHDKLDPEDCSIXGLYRLIWNVSXSHSILFIRIGMDCSQPOXIFACHSPFEYFSCFGLH  
410 420 430 440 450 460 470 480 490 500  
MAPGLASAVL---LLILCCAGS---GFCGKVLVWPCENSHWL-  
510 520 530 540 550 560  
VSYVIRKLITKGNSHHRDPMV-----NSFIDPIHSTMSDSRFGGATK---TILGYPILIOPSIGSXCG  
510 520 530 540 550 560  
-----NLKTLLEELVKGHEVYVLTLSNNLFDYNRHDAFNEFVLPVPTDRNMSENILNEFI-----







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